

Figure 1

Map of Human CD20/IgE-Receptor Like cDNA (SEQ ID NO: 1) and
Amino Acid Sequence (SEQ ID NO: 2)
(Aqp-96614-a1)
(CD20RP2)

5

1	TTCCAGTGCTCCAGGCAGCCTCAGCACAAGAAAAGAACATGGTCTAGACTGAAGTACCAA	60
61	CTAAATCATCTCCTTTCAAATTTATCACCGACACCATCATGGATTCAAGCACCGCACACAG	120
1	M D S S T A H S	8
121	TCCGGTGTTTCTGGTATTTCTCCAGAAATCACTGCTTCAGAATATGAGTCCACAGAACT	180
9	P V F L V F P P E I T A S E Y E S T E L	28
181	TTCAGCCACGACCTTTTCAACTCAAAGCCCCTTGCAAAAATTTATTGCTAGAAAAATGAA	240
29	S A T T F S T Q S P L Q K L F A R K M K	48
241	AATCTTAGGGACTATCCAGATCCTGTTTGGAAATTGACCTTTCTTTTGGAGTTATCTT	300
49	I L G T I Q I L F G I M T F S F G V I F	68
301	CCTTTTCACTTTGTAAAACCATATCCAAGTTTCCCTTTTATTTCTTTTCAGGATATCC	360
69	L F T L L K P Y P R F P F I F L S G Y P	88
361	ATTCTGGGGCTCTGTTTTGTTCATTAACTTGGAGCCTTCTTAATGTCAGTGAAAAGAAA	420
89	F W G S V L F I N S G A F L I A V K R K	108
421	AACCACAGAACTCTGATAATATTGAGCCGAATAATGAATTTTCTTAGTGCCCTGGGAGC	480
109	T T E T L I I L S R I M N F L S A L G A	128
481	AATAGCTGGAATCATTTCTCCTCACATTGGTTTCATCTAGATCAAAACTACATTGTGG	540
129	I A G I I L L T F G F I L D Q N Y I C G	148
541	TTATTCTACCAAAATAGTCAGTGAAGGCTGTACTGTCTCTTGGGAATTTTGAT	600
149	Y S H Q N S Q C K A V T V L F L G I L I	168
601	TACATTGATGACTTTTCAGCATTATTGAATTATTCAITTTCTCTGCCTTTCTCAATTTTGGG	660
169	T L M T F S I I E L F I S L P F S I L G	188
661	GTGCCACTCAGAGGATTGTGATTGTGAACAATGTTGTTGACTAGCACTGTGAGAATAAAG	720
189	C H S E D C D C E Q C C *	201
721	ATGTGTTAAATCTCAAAAAAAAAAAAAAAAAAAAAA	760

Figure 2

Map of Human CD20/IgE-receptor Like cDNA (SEQ ID NO: 3) and
Amino Acid Sequence (SEQ ID NO: 4)

(Agp-69406-al)
(CD20RPl)

	1	GGCAGGAACAGCCAGTGGGAGGTTCCAGCTGAGCGCTCCCCAGAGGTGAGCTGATCCCCA	60
	61	GCCACAGCACACAGGACCAGGCTGCAGAGAACGATCATCAGCATCATGCTATTACAATC	120
10	1		5
		M L L Q S	
	121	CCAAACCATGGGGGTTTCTCACAGCTTTACACCAAAGGGCATCACTATCCCTCAAAGAGA	180
	6	Q T M G V S H S F T P K G I T I P Q R E	25
	181	GAAACCTGGACACATGTACCAAAACGAAGATTACCTGCAGAACGGGCTGCCAACAGAAAC	240
	26	K P G H M Y Q N E D Y L Q N G L P T E T	45
15	241	CACCGTTCTTGGGACTGTCCAGATCCTGTGTGCTGTGTTGATTTCAGTCTGGGGGCCAT	300
	46	T V L G T V Q I L C C L L I S S L G A I	65
	301	CTTGGTTTTTGTCTCCCTACCCCTCCCACTTCAATCCAGCAATTTCCACCACCTTTGATGTC	360
	66	L V F A P Y P S H F N P A I S T T L M S	85
20	361	TGGGTACCCATTTTTAGGAGCTCTGTGTTTTGGCATTACTGGATCCCTCTCAATTATCTC	420
	86	G Y P F L G A L C F G I T G S L S I I S	105
	421	TGGAACAATCAACTAAGCCCTTTGACCTGAGCAGCTTGACCTCAAATGCAGTGAGTTC	480
	106	G K Q S T K P F D L S S L T S N A V S S	125
	481	TGTTACTGCAGGAGCAGCCCTCTTCCTCTGTGACAGCATGGTAGCCCTGAGGACTGC	540
	126	V T A G A G L F L L A D S M V A L R T A	145
25	541	CTCTCAACATTGTGGCTCAGAAATGGATTATCTATCCTCATTGCCTTATTCGGAGTACTA	600
	146	S Q H C G S E M D Y L S S L P Y S E Y Y	165
	601	TTATCCAATATATGAAATCAAAGATTGTCTCCTGACCAGTGTCAGTTTAACAGGTGTCCT	660
	166	Y P I Y E I K D C L L T S V S L T G V L	185
30	661	AGTGTGATGCTCATCTTCACTGTGTGGAGCTCTTATTAGTCATACAGTCTGTCTT	720
	186	V V M L I F T V L E L L L A A Y S S V F	205
	721	TTGGTGGAAACAGCTCTACTCCAACAACCTGGGAGTTCATTTTCTCGACCCAGTCACA	780
	206	W W K Q L Y S N N P G S S F S S T Q S Q	225
	781	AGATCATATCCAACAGGTCAAAAAGAGTCTTACGGTCTTGGATATAAGTAACCTTTGG	840
	226	D H I Q Q V K K S S S R S W I *	241
35	841	CCTCAGAGGAAGGAAAGCAACTCAACACTCATGGTCAAGTGATGATAGACTTTCCTGAA	900
	901	ATCTCTGCCATTTTAGATACTGTGAAACAACTAAAAAAGCTTTTGTGTTGTATT	960
	961	GAAAAAAAAAAAAAAAAAAAAA	982

